



SEQUENCE LISTING

<110> MORI, SATOSHI
NAKANISHI, HIROMI
OKI, HIROYUKI
YAMAGUCHI, HIROTAKA

<120> METHOD FOR TRANSFORMING PLANT, THE RESULTANT PLANT AND
GENE THEREOF

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<140> 10/625,821
<141> 2003-07-22

<150> 09/646,825
<151> 2000-09-22

<150> JP/10-96637
<151> 1998-03-24

<160> 38

<170> PatentIn Ver. 2.1

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<223> Description of Artificial Sequence: Synthetic
saccharomyces cerevisiae

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<222> (20)..(2077)

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Ile Ser Phe Ala Thr Val Gln Ser Ser Ala Thr Leu Ile Ser Thr
15 20 25

tca tgc att tct cag gct gca ctg tac cag ttc gga tgc tca agc aag 148
Ser Cys Ile Ser Gln Ala Ala Leu Tyr Gln Phe Gly Cys Ser Ser Lys
30 35 40

tca aag tct tgc tac tgc aag aac atc aat tgg ctc gga agc gtc act 196
Ser Lys Ser Cys Tyr Cys Lys Asn Ile Asn Trp Leu Gly Ser Val Thr
45 50 55

gca tgc gct tat gag aac tcc aaa tct aac aag act ctg gac tcc gct 244
Ala Cys Ala Tyr Glu Asn Ser Lys Ser Asn Lys Thr Leu Asp Ser Ala
60 65 70 75

ttg atg aaa ctt gcc agc caa tgc tca agt atc aag gtt tac aca ctg	292
Leu Met Lys Leu Ala Ser Gln Cys Ser Ser Ile Lys Val Tyr Thr Leu	
80 85 90	
gag gac atg aag aac atc tac ctt aat gca agt aac tac ctt cgc gct	340
Glu Asp Met Lys Asn Ile Tyr Leu Asn Ala Ser Asn Tyr Leu Arg Ala	
95 100 105	
cct gag aaa tcc gat aag aag aca gtt gtt tca caa ccg ttg atg gca	388
Pro Glu Lys Ser Asp Lys Lys Thr Val Val Ser Gln Pro Leu Met Ala	
110 115 120	
aat gag acg gcc tat cac tac tac tat gag gaa aac tat ggg atc cac	436
Asn Glu Thr Ala Tyr His Tyr Tyr Glu Glu Asn Tyr Gly Ile His	
125 130 135	
ttg aat ttg atg cga tct caa tgg tgc gca tgg ggc ctc gtc ttc ttc	484
Leu Asn Leu Met Arg Ser Gln Trp Cys Ala Trp Gly Leu Val Phe Phe	
140 145 150 155	
tgg gtc gca gtc ctt acc gcc gca act atc ttg aac att ctc aaa cgc	532
Trp Val Ala Val Leu Thr Ala Ala Thr Ile Leu Asn Ile Leu Lys Arg	
160 165 170	
gta ttc ggc aag aac att atg gca aat tct gtt aag aag tct ctt atc	580
Val Phe Gly Lys Asn Ile Met Ala Asn Ser Val Lys Lys Ser Leu Ile	
175 180 185	
tac cca agc gtt tac aaa gac tac aac gag aga act ttc tat ctt tgg	628
Tyr Pro Ser Val Tyr Lys Asp Tyr Asn Glu Arg Thr Phe Tyr Leu Trp	
190 195 200	
aaa cgt ttg cca ttc aac ttt aca act cga ggc aaa gga ctc gta gtt	676
Lys Arg Leu Pro Phe Asn Phe Thr Thr Arg Gly Lys Gly Leu Val Val	
205 210 215	
ctt atc ttt gtc att ctg act att ctc tca ctc tct ttc gga cat aac	724
Leu Ile Phe Val Ile Leu Thr Ile Leu Ser Leu Ser Phe Gly His Asn	
220 225 230 235	
atc aag ttg cca cat cct tac gat aga cct aga tgg aga aga tca atg	772
Ile Lys Leu Pro His Pro Tyr Asp Arg Pro Arg Trp Arg Arg Ser Met	
240 245 250	
gca ttc gtc tca cgc cgt gct gac ttg atg gca atc gct ctt ttc ccc	820
Ala Phe Val Ser Arg Arg Ala Asp Leu Met Ala Ile Ala Leu Phe Pro	
255 260 265	
gtg gtg tac ctt ttc ggt atc cgg aac aac ccc ttc atc cca atc acc	868
Val Val Tyr Leu Phe Gly Ile Arg Asn Asn Pro Phe Ile Pro Ile Thr	
270 275 280	
gga ttg agc ttt agt act ttc aac ttt tac cac aaa tgg tca gca tac	916
Gly Leu Ser Phe Ser Thr Phe Asn Phe Tyr His Lys Trp Ser Ala Tyr	
285 290 295	

gtc tgc ttc atg tta gcc gtc gtc cat tca atc gtt atg acc gct tca	964
Val Cys Phe Met Leu Ala Val Val His Ser Ile Val Met Thr Ala Ser	
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gga gtt aaa cga gga gta ttc cag tct ctt gta agg aaa ttc tac ttc	1012
Gly Val Lys Arg Gly Val Phe Gln Ser Leu Val Arg Lys Phe Tyr Phe	
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aga tgg gga ata gta gcc aca att ctt atg tcc atc atc att ttc cag	1060
Arg Trp Gly Ile Val Ala Thr Ile Leu Met Ser Ile Ile Ile Phe Gln	
335 340 345	
tcc gag aag gtc ttc agg aac cga ggt tat gaa atc ttc tta ctt att	1108
Ser Glu Lys Val Phe Arg Asn Arg Gly Tyr Glu Ile Phe Leu Leu Ile	
350 355 360	
cac aaa gcc atg aac atc atg ttt atc ata gct atg tat tac cat tgc	1156
His Lys Ala Met Asn Ile Met Phe Ile Ile Ala Met Tyr Tyr His Cys	
365 370 375	
cac aca cta gga tgg atg ggc tgg atc tgg tcc atg gct ggc atc ctc	1204
His Thr Leu Gly Trp Met Gly Trp Ile Trp Ser Met Ala Gly Ile Leu	
380 385 390 395	
tgc ttc gac agg ttc tgc cga att gta cgt atc atc atg aac gga ggt	1252
Cys Phe Asp Arg Phe Cys Arg Ile Val Arg Ile Ile Met Asn Gly Gly	
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ctt aag acc gcc act ttg tcg acc aca gat gat tct aac gtt atc aag	1300
Leu Lys Thr Ala Thr Leu Ser Thr Thr Asp Asp Ser Asn Val Ile Lys	
415 420 425	
atc tct gtc aag aag cct aag ttc ttc aag tat caa gtg gga gca ttt	1348
Ile Ser Val Lys Lys Pro Lys Phe Phe Lys Tyr Gln Val Gly Ala Phe	
430 435 440	
gcc tat atg tac ttt ctt tca cca aaa tca gcc tgg ttc tac agt ttt	1396
Ala Tyr Met Tyr Phe Leu Ser Pro Lys Ser Ala Trp Phe Tyr Ser Phe	
445 450 455	
caa tct cat ccc ttc aca gtc cta tca gaa agg cac aga gat cct aac	1444
Gln Ser His Pro Phe Thr Val Leu Ser Glu Arg His Arg Asp Pro Asn	
460 465 470 475	
aac cca gat caa cta act atg tac gtc aaa gct aac aag ggc att acg	1492
Asn Pro Asp Gln Leu Thr Met Tyr Val Lys Ala Asn Lys Gly Ile Thr	
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aga gta ctt ctt agc aaa gtt cta agc gct cca aac cat acc gtt gat	1540
Arg Val Leu Leu Ser Lys Val Leu Ser Ala Pro Asn His Thr Val Asp	
495 500 505	
tgc aag att ttc tta gag gga cca tat ggc gta act gtc cct cac att	1588
Cys Lys Ile Phe Leu Glu Gly Pro Tyr Gly Val Thr Val Pro His Ile	
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gcc aaa ctt aag aga aat cta gta gga gta gct gcg ggc ctc ggc gtg	1636
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525 530 535	
gca gcc atc tac ccc cat ttc gta gaa tgc ctt aga ttg cct agc act	1684
Ala Ala Ile Tyr Pro His Phe Val Glu Cys Leu Arg Leu Pro Ser Thr	
540 545 550 555	
gat caa ctg cag cac aag ttc tac tgg atc gtc aac gac ctt agt cac	1732
Asp Gln Leu Gln His Lys Phe Tyr Trp Ile Val Asn Asp Leu Ser His	
560 565 570	
ctt aag tgg ttc gaa aac gag cta caa tgg ctt aag gag aaa tct tgt	1780
Leu Lys Trp Phe Glu Asn Glu Leu Gln Trp Leu Lys Glu Lys Ser Cys	
575 580 585	
gaa gtc tct gtc atc tac act ggg tca tca gtg gag gat aca aac tca	1828
Glu Val Ser Val Ile Tyr Thr Gly Ser Ser Val Glu Asp Thr Asn Ser	
590 595 600	
gat gag tcc act aag ggt ttc gat gac aag gaa gaa tct gaa atc acc	1876
Asp Glu Ser Thr Lys Gly Phe Asp Asp Lys Glu Glu Ser Glu Ile Thr	
605 610 615	
gta gaa tgc ctt aac aag agg cca gac ctc aaa gag cta gtg aga tca	1924
Val Glu Cys Leu Asn Lys Arg Pro Asp Leu Lys Glu Leu Val Arg Ser	
620 625 630 635	
gag atc aaa ttg tca gaa ctc gag aac aac aac atc act ttc tac tca	1972
Glu Ile Lys Leu Ser Glu Leu Glu Asn Asn Ile Thr Phe Tyr Ser	
640 645 650	
tgc gga cca gcg act ttc aat gac gac ttt agg aat gca gtt gta caa	2020
Cys Gly Pro Ala Thr Phe Asn Asp Asp Phe Arg Asn Ala Val Val Gln	
655 660 665	
ggt atc gat tct agt ctg aag ata gat gtc gaa cta gag gag gag agt	2068
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Ala Ala Leu Tyr Gln Phe Gly Cys Ser Ser Lys Ser Lys Ser Cys Tyr
 35 40 45

Cys Lys Asn Ile Asn Trp Leu Gly Ser Val Thr Ala Cys Ala Tyr Glu
 50 55 60

Asn Ser Lys Ser Asn Lys Thr Leu Asp Ser Ala Leu Met Lys Leu Ala
 65 70 75 80

Ser Gln Cys Ser Ser Ile Lys Val Tyr Thr Leu Glu Asp Met Lys Asn
 85 90 95

Ile Tyr Leu Asn Ala Ser Asn Tyr Leu Arg Ala Pro Glu Lys Ser Asp
 100 105 110

Lys Lys Thr Val Val Ser Gln Pro Leu Met Ala Asn Glu Thr Ala Tyr
 115 120 125

His Tyr Tyr Tyr Glu Glu Asn Tyr Gly Ile His Leu Asn Leu Met Arg
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Ser Gln Trp Cys Ala Trp Gly Leu Val Phe Phe Trp Val Ala Val Leu
 145 150 155 160

Thr Ala Ala Thr Ile Leu Asn Ile Leu Lys Arg Val Phe Gly Lys Asn
 165 170 175

Ile Met Ala Asn Ser Val Lys Lys Ser Leu Ile Tyr Pro Ser Val Tyr
 180 185 190

Lys Asp Tyr Asn Glu Arg Thr Phe Tyr Leu Trp Lys Arg Leu Pro Phe
 195 200 205

Asn Phe Thr Thr Arg Gly Lys Gly Leu Val Val Leu Ile Phe Val Ile
 210 215 220

Leu Thr Ile Leu Ser Leu Ser Phe Gly His Asn Ile Lys Leu Pro His
 225 230 235 240

Pro Tyr Asp Arg Pro Arg Trp Arg Arg Ser Met Ala Phe Val Ser Arg
 245 250 255

Arg Ala Asp Leu Met Ala Ile Ala Leu Phe Pro Val Val Tyr Leu Phe
 260 265 270

Gly Ile Arg Asn Asn Pro Phe Ile Pro Ile Thr Gly Leu Ser Phe Ser
 275 280 285

Thr Phe Asn Phe Tyr His Lys Trp Ser Ala Tyr Val Cys Phe Met Leu
 290 295 300

Ala Val Val His Ser Ile Val Met Thr Ala Ser Gly Val Lys Arg Gly
 305 310 315 320

Val Phe Gln Ser Leu Val Arg Lys Phe Tyr Phe Arg Trp Gly Ile Val
 325 330 335

Ala Thr Ile Leu Met Ser Ile Ile Ile Phe Gln Ser Glu Lys Val Phe
 340 345 350

Arg Asn Arg Gly Tyr Glu Ile Phe Leu Leu Ile His Lys Ala Met Asn
 355 360 365

Ile Met Phe Ile Ile Ala Met Tyr Tyr His Cys His Thr Leu Gly Trp
 370 375 380

Met Gly Trp Ile Trp Ser Met Ala Gly Ile Leu Cys Phe Asp Arg Phe
 385 390 395 400

Cys Arg Ile Val Arg Ile Ile Met Asn Gly Gly Leu Lys Thr Ala Thr
 405 410 415

Leu Ser Thr Thr Asp Asp Ser Asn Val Ile Lys Ile Ser Val Lys Lys
 420 425 430

Pro Lys Phe Phe Lys Tyr Gln Val Gly Ala Phe Ala Tyr Met Tyr Phe
 435 440 445

Leu Ser Pro Lys Ser Ala Trp Phe Tyr Ser Phe Gln Ser His Pro Phe
 450 455 460

Thr Val Leu Ser Glu Arg His Arg Asp Pro Asn Asn Pro Asp Gln Leu
 465 470 475 480

Thr Met Tyr Val Lys Ala Asn Lys Gly Ile Thr Arg Val Leu Leu Ser
 485 490 495

Lys Val Leu Ser Ala Pro Asn His Thr Val Asp Cys Lys Ile Phe Leu
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Glu Gly Pro Tyr Gly Val Thr Val Pro His Ile Ala Lys Leu Lys Arg
 515 520 525

Asn Leu Val Gly Val Ala Ala Gly Leu Gly Val Ala Ala Ile Tyr Pro
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His Phe Val Glu Cys Leu Arg Leu Pro Ser Thr Asp Gln Leu Gln His
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Lys Phe Tyr Trp Ile Val Asn Asp Leu Ser His Leu Lys Trp Phe Glu
 565 570 575

Asn Glu Leu Gln Trp Leu Lys Glu Lys Ser Cys Glu Val Ser Val Ile
 580 585 590

Tyr Thr Gly Ser Ser Val Glu Asp Thr Asn Ser Asp Glu Ser Thr Lys
 595 600 605

Gly Phe Asp Asp Lys Glu Glu Ser Glu Ile Thr Val Glu Cys Leu Asn
 610 615 620

Lys Arg Pro Asp Leu Lys Glu Leu Val Arg Ser Glu Ile Lys Leu Ser
 625 630 635 640

Glu Leu Glu Asn Asn Asn Ile Thr Phe Tyr Ser Cys Gly Pro Ala Thr
 645 650 655

Phe Asn Asp Asp Phe Arg Asn Ala Val Val Gln Gly Ile Asp Ser Ser
 660 665 670

Leu Lys Ile Asp Val Glu Leu Glu Glu Ser Phe Thr Trp
 675 680 685

<210> 3
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<220>
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<210> 4
 <211> 24
 <212> DNA
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 <223> Description of Artificial Sequence: Primer

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<210> 5
 <211> 83
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Primer

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ttcggatgtt caagcaagtc aaa 83

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<212> DNA
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<220>
<223> Description of Artificial Sequence: Primer

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gcgcattatgtt gaactccaaa tct 83

<210> 8
<211> 83
<212> DNA
<213> Artificial Sequence

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<223> Description of Artificial Sequence: Primer

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agagtcttgtt tagatttggaa gtt 83

<210> 9
<211> 83
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

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cttcatgtcc tccagtgtgtt aaa 83

<210> 10
<211> 83
<212> DNA
<213> Artificial Sequence

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<223> Description of Artificial Sequence: Primer

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gtgaaacaac tgtcttcata tcg 83

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<211> 80
<212> DNA
<213> Artificial Sequence

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<223> Description of Artificial Sequence: Primer

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tcgcagtcctt taccggcgca 80

<210> 12
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<212> DNA
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<223> Description of Artificial Sequence: Primer

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aaattctgtt aagaagtctc 80

<210> 13
<211> 80
<212> DNA
<213> Artificial Sequence

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<223> Description of Artificial Sequence: Primer

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ctttggaaac gttgccatt 80

<210> 14
<211> 80
<212> DNA
<213> Artificial Sequence

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<223> Description of Artificial Sequence: Primer

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taaagggttggaaacacgt 80

<210> 15
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<212> DNA
<213> Artificial Sequence

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<223> Description of Artificial Sequence: Primer

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gtgagacgaa tgccattgat 80

<210> 17
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<212> DNA
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<220>
<223> Description of Artificial Sequence: Primer

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acaaatggtc agcatacgtc tgc 83

<210> 18
<211> 83
<212> DNA
<213> Artificial Sequence

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<223> Description of Artificial Sequence: Primer

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aaacgaggag tattccagtc tct 83

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<211> 83
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<223> Description of Artificial Sequence: Primer

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<210> 20
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<210> 21
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<212> DNA
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<223> Description of Artificial Sequence: Primer

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<210> 22
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<223> Description of Artificial Sequence: Primer

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<210> 23
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<212> DNA
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<223> Description of Artificial Sequence: Primer

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<210> 25
<211> 82
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<223> Description of Artificial Sequence: Primer

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<210> 26
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<210> 27
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<223> Description of Artificial Sequence: Primer

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<210> 28
<211> 82
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<223> Description of Artificial Sequence: Primer

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<210> 29
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<223> Description of Artificial Sequence: Primer

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gagctacaat ggcttaa 77

<210> 30
<211> 77
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<223> Description of Artificial Sequence: Primer

<400> 30
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ggatacaaaac tcagatg 77

<210> 31
<211> 77
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 31
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aatgcctaa caagagg 77

<210> 32
<211> 77
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer

<400> 32
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tctggccctct tgttaag 77

<210> 33
<211> 77
<212> DNA
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<220>
<223> Description of Artificial Sequence: Primer

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agaaggatgtat gttgttgc 77

<210> 34
<211> 77
<212> DNA
<213> Artificial Sequence

<220>
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agaatcgata cttgtat 77

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<211> 2059
<212> DNA
<213> *Saccharomyces cerevisiae*

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Ser Leu Ser Phe Gly His Asn Ile Lys Leu Pro His
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